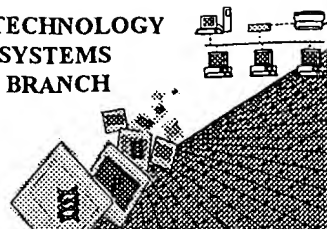


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/857,613
Source: PL/09
Date Processed by STIC: 2/13/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/857,613

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,613

DATE: 02/13/2002

TIME: 10:08:24

Input Set : A:\BB1289 PCT seq 1st.txt

Output Set: N:\CRF3\02132002\I857613.raw

Does Not Comply
Corrected Diskette Needed

pp 1-7, 9

3 <110> APPLICANT: Rafalski, J. Antoni
4 Cahoon, Rebecca E.
5 Coughlan, Sean
6 Miao, Guo-Hua
8 <120> TITLE OF INVENTION: PLANT VITAMIN E BIOSYNTHETIC ENZYMES
10 <130> FILE REFERENCE: BB1289
12 <140> CURRENT APPLICATION NUMBER: US/09/857,613
13 <141> CURRENT FILING DATE: 2002-01-14
15 <150> PRIOR APPLICATION NUMBER: 60/110,781
16 <151> PRIOR FILING DATE: 1998-12-03
18 <160> NUMBER OF SEQ ID NOS: 43
20 <170> SOFTWARE: Microsoft Office 97

ERRORED SEQUENCES

22 <210> SEQ ID NO: 1
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25 <213> ORGANISM: Zea mays
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29 tcagggttact ctgcaagttg ctgatgctct ggagcaaccg ttctctgacg ggcagttcga 120
30 tctggtgtgg tccatggaga gtggcgagca catgccggac aagagaaagt ttgttagtga 180
31 gctagcacgc gtggcggtc ctggaggac aataatcatc gtgacatggt gccataggaa 240
32 cctggatcca tccgaaacct cgctaaagcc cgatgaactg agcctcctga ggaggatatg 300
33 cgacgcgtac tacctcccg actggtgctc accttcagac tatgtgaaca ttgccaagtc 360
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E--> 37 catcaaatc accatcatca cctgtcgcaa gcctggagcc gcgtanagg aggcaaggag 600
38 cacaagttac taqcacagca caggatgcaa gtgcatatgt agatcatggc acatcgccgt 660
E--> 39 cactcatcat actgcacaaa atcaaatctc caggacattt aataattctg cacctcanat 720
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93 gatgagctga atctcctgaa aaggatatgc gatgcatatt atctcccaga ctggtgctct 180

*see
item 9 on
Error
Summary
Sheet*

p. 2

RAW SEQUENCE LISTING

DATE: 02/13/2002

PATENT APPLICATION: US/09/857,613

TIME: 10:08:24

Input Set : A:\BB1289 PCT seq 1st.txt

Output Set: N:\CRF3\02132002\I857613.raw

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E--> 96 gnaaggggta actttctcct ggctaagaan tgggtgggaa gacgattaag aaggtggaat 360
E--> 97 ggggtgatgcc tccggatgat nnaaggntac aaagaaangg gtcaacaaat ttaacaanaa 420
E--> 98 caacctgtnc caaagncctg aaacaacgca ataatacccc antaatnaaa ttncgctcct 480
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see item 9

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130 <400> SEQUENCE: 5

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133 gcctcggctt cccctcgccg cgccctctgc ctccaccacc accgcccgcg ccgcccgcagc 180
134 agccggagga cgaaactcgc cgtgcgcgcg atggcaccga cgttgctctc gtcgtcgacg 240
E--> 135 gcggcggcag ctcccccggg gctgaaggag ggcacgcggg ggctctacga cgaancgtcc 300
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138 gccgcctccc cgatgatcgg agaagaacca aaatgtattg atttggtgtg gattggtggt 480
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item 9

item 9

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145 <213> ORGANISM: Oryza sativa

147 <400> SEQUENCE: 6

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154 Arg Cys Thr Ser Arg His Leu Cys Ala Ser Ala Ser Pro Arg Ala Gly
155 35 40 45
157 Leu Cys Leu His His His Arg Arg Arg Arg Ser Ser Arg Arg Thr
158 50 55 60
160 Lys Leu Ala Val Arg Ala Met Ala Pro Thr Leu Ser Ser Ser Ser Thr
161 65 70 75 80
163 Ala Ala Ala Ala Pro Gly Leu Lys Glu Gly Ile Ala Gly Leu Tyr
164 85 90 95
E--> 166 Asp Glu Xaa Ser Gly Val Trp Glu Ser Ile Trp Gly Glu His Met His
167 100 105 110
169 His Gly Phe Tyr Asp Ala Gly Glu Gly Ala Ser Met Ser Asp His Arg
170 115 120 125
172 Arg Ala Pro Val Arg Met Ile Glu Asp Leu Ala Phe Ala Ala Ser Pro
173 130 135 140

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item 9

277 <210> SEQ ID NO: 9

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279 <212> TYPE: DNA

280 <213> ORGANISM: Triticum aestivum

282 <400> SEQUENCE: 9

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,613

DATE: 02/13/2002

TIME: 10:08:24

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Output Set: N:\CRF3\02132002\I857613.raw

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284 actccggcga ggccgcctcc atgtccgacc accgcccgcg ccagatccgc atgatcgagg 120
285 aggccctcgc cttcgccgcc gtccccgacg atccgacaaa caaacccaaa acgattgttg 180
286 atgttgatg cggaatcggg ggtagctcaa gatacctggg cgaacaaata tggagcacia 240
287 tgctctggga tcacattgac ccagtgcagg ctgagagagg aaatgccctc gcggcagcgc 300
288 aaggggttgt ccggacaagg ttctttccaa ttgctgatct ctgggagcaa ccatttctctg 360
E--> 289 gatgggcatt tgatcttgtc cgggnccatg ggagantggt gacacatgcc gaacaaacag 420
290 aagtttgtaa gcgagctggc acgcgtcgca gctccaggag caactatcat catcgtgacc 480
291 tggtgccata ggaacctcgc gccatcggag gactcactga aacctgacga gctgaatctt 540
292 ttgaaaaaga tttgtgatgc atattacctc ccggattggt gctctccctc ggattatgtc 600
293 aagattgccg agtcattgtc tcttgaggat atcaaaacgg ccgactggtc tgaaaacgtg 660
294 gccccgttct ggccgtgctg catccaatca gcaactgacat ggaaaggcct cacttctcta 720
295 ctaaggagtg gatggaagac gataaaggga gcaactggtg tgccctctcat gatccaaggc 780
296 tacaagaaag gcctcattaa gttcaagcat catcacctgc cacaaacccc aagcagccat 840
297 agaaggagaa cctggaggcc gcacgcacca agagtggtag aatagaacca tgtgattgga 900
E--> 298 atagactcng cttgctgtcg ccttggtagc tgaataattc gtgttaccgt gcctctgtat 960
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302 <211> LENGTH: 293
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310 Gly Phe Tyr Asp Ser Gly Glu Ala Ala Ser Met Ser Asp His Arg Arg
311 20 25 30
313 Ala Gln Ile Arg Met Ile Glu Glu Ala Leu Ala Phe Ala Ala Val Pro
314 35 40 45
316 Asp Asp Pro Thr Asn Lys Pro Lys Thr Ile Val Asp Val Gly Cys Gly
317 50 55 60
319 Ile Gly Gly Ser Ser Arg Tyr Leu Gly Glu Gln Ile Trp Ser Thr Met
320 65 70 75 80
322 Leu Trp Asp His Ile Asp Pro Val Gln Ala Glu Arg Gly Asn Ala Leu
323 85 90 95
325 Ala Ala Ala Gln Gly Val Val Arg Thr Arg Phe Phe Pro Ile Ala Asp
326 100 105 110
E--> 328 Leu Trp Glu Gln Pro Phe Pro Gly Trp Ala Phe Asp Leu Val Xaa Xaa
329 115 120 125
E--> 331 Xaa Xaa Xaa Xaa Xaa His Met Pro Asn Lys Gln Lys Phe Val Ser Glu
332 130 135 140
334 Leu Ala Arg Val Ala Ala Pro Gly Ala Thr Ile Ile Ile Val Thr Trp
335 145 150 155 160
337 Cys His Arg Asn Leu Ala Pro Ser Glu Asp Ser Leu Lys Pro Asp Glu
338 165 170 175
340 Leu Asn Leu Leu Lys Lys Ile Cys Asp Ala Tyr Tyr Leu Pro Asp Trp
341 180 185 190
343 Cys Ser Pro Ser Asp Tyr Val Lys Ile Ala Glu Ser Leu Ser Leu Glu
344 195 200 205
346 Asp Ile Lys Thr Ala Asp Trp Ser Glu Asn Val Ala Pro Phe Trp Pro

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,613

DATE: 02/13/2002

TIME: 10:08:24

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350 225      230      235      240
352 Arg Ser Gly Trp Lys Thr Ile Lys Gly Ala Leu Val Met Pro Leu Met
353      245      250      255
355 Ile Gln Gly Tyr Lys Lys Gly Leu Ile Lys Phe Lys His His His Leu
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362      290
364 <210> SEQ ID NO: 11
365 <211> LENGTH: 432
366 <212> TYPE: DNA
367 <213> ORGANISM: Oryza sativa
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371 gggcgcgccg ctgcgcgcca ggtccgacct ctccacgggg aactccgcgc acgcctccct 120
372 cctcctccgc tcgcctccg tcgcgttcct ctccacggcc ccctacggcg gcgaccacgg 180
373 cgtcggcgcg gacgcggcca ccaccgcctc catcccttcc ttctccctt cctttctccc 240
374 cgctcctgga tcaggccaca ggaggggagc gatggtggag gcggccaccg taggcggcgg 300
375 aggtggcggt cctcctccct agctcccaga cccggctgga ggagggagtg atggtggcgg 360
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408 ggacgtgggc accgcccaga gcggcctcaa ctccggtgtg ctgcgcaaca acgcccagag 180
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410 gtacctggac caccacggcg qcccgggggg gcagcacatc gcgctggcca gcgacgacgt 300
E--> 411 gctcgggacg ctganggaga tgcngggcgc ctccgcatgg gcggttcgat tcttggggcc 360
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E--> 413 taacaatgcc aagactcngg tgcctggac aaggatacaa gggtttccaa tnttaacaag 480
E--> 414 cattgaanag nnactttctg gngagatcaa gatggtgatg aaagtnaatg gaagntncaa 540
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419 <211> LENGTH: 123
420 <212> TYPE: PRT
421 <213> ORGANISM: Oryza sativa
423 <400> SEQUENCE: 14
424 Tyr Gly Leu Arg Arg Phe Asp His Val Val Gly Asn Val Pro Glu Leu
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427 Ala Pro Val Ala Ala Tyr Ile Ser Gly Phe Thr Gly Phe His Glu Phe
428 20 25 30

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,613

DATE: 02/13/2002

TIME: 10:08:24

Input Set : A:\BB1289 PCT seq 1st.txt

Output Set: N:\CRF3\02132002\I857613.raw

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430 Ala Glu Phe Thr Ala Glu Asp Val Gly Thr Ala Glu Ser Gly Leu Asn
431      35      40      45
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434      50      55      60
436 Glu Pro Val His Gly Thr Lys Arg Arg Ser Gln Ile Gln Thr Tyr Leu
437 65      70      75      80
439 Asp His His Gly Gly Pro Gly Val Gln His Ile Ala Leu Ala Ser Asp
440      85      90      95
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446      115      120
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450 <212> TYPE: DNA
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453 <400> SEQUENCE: 15
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456 taagtcggac cgctttcaag tcaaccgctt ccaccacatc gagttctggt gcaccgatgc 180
457 caccaacgcc tctcgccgat tctcttgagg acttggaatg cctattgttg caaaatctga 240
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459 cctctttctc gctccttact ctcctctctt ctccgcggc tctcccgctg cctcctccgc 360
460 ctccattccc agtttcgacg ccgccacctg ccttgcttc gctgccaac acggttcgg 420
461 cgtccgcgcc atcgcttgga agtcgccga cgcggaagcc gctttcagcg ccagcgtcgc 480
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item 9

item 9

p.6

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474 <211> LENGTH: 276
475 <212> TYPE: PRT
476 <213> ORGANISM: Glycine max
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483      20      25      30
485 Arg Thr Asn Pro Lys Ser Asp Arg Phe Gln Val Asn Arg Phe His His
486      35      40      45
488 Ile Glu Phe Trp Cys Thr Asp Ala Thr Asn Ala Ser Arg Arg Phe Ser
489      50      55      60
491 Trp Gly Leu Gly Met Pro Ile Val Ala Lys Ser Asp Leu Ser Thr Gly

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RAW SEQUENCE LISTING

DATE: 02/13/2002

PATENT APPLICATION: US/09/857,613

TIME: 10:08:24

Input Set : A:\BB1289 PCT seq 1st.txt

Output Set: N:\CRF3\02132002\I857613.raw

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495          85          90          95
497 Leu Phe Ser Ala Pro Tyr Ser Pro Ser Leu Ser Ala Gly Ser Ser Ala
498          100          105          110
500 Ala Ser Ser Ala Ser Ile Pro Ser Phe Asp Ala Ala Thr Cys Leu Ala
501          115          120          125
503 Phe Ala Ala Lys His Gly Phe Gly Val Arg Ala Ile Ala Leu Glu Val
504          130          135          140
506 Ala Asp Ala Glu Ala Ala Phe Ser Ala Ser Val Ala Lys Gly Ala Glu
507 145          150          155          160
509 Pro Ala Ser Pro Pro Val Leu Val Asp Asp Arg Thr Gly Phe Ala Glu
510          165          170          175
512 Val Arg Leu Tyr Gly Asp Val Val Leu Arg Tyr Val Ser Tyr Lys Asp
513          180          185          190
E--> 515 Ala Ala Pro Gln Ala Pro His Ala Asp Xaa Ser Arg Trp Phe Leu Pro item 9
516          195          200          205
518 Gly Phe Glu Ala Ala Ala Ser Ser Ser Phe Pro Glu Leu Asp Tyr
519          210          215          220
521 Gly Ile Arg Arg Leu Asp His Ala Val Gly Asn Val Pro Glu Leu Ala
522 225          230          235          240
524 Pro Ala Val Arg Tyr Leu Lys Gly Phe Ser Gly Phe His Glu Phe Ala
525          245          250          255
527 Glu Phe Thr Ala Glu Asp Val Gly Thr Ser Glu Ser Gly Leu Asn Ser
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530 Val Val Leu Ala
531          275
533 <210> SEQ ID NO: 17
534 <211> LENGTH: 511
535 <212> TYPE: DNA
536 <213> ORGANISM: Vernonia mesipifolia
538 <400> SEQUENCE: 17
539 ccacaccgat tgccggaact tcaccgcctc tcacggcctt gcagtcgag caatcgccat 60
540 tgaagtcgat gacgccgaat tagctttctc cgtcagcgtc tctcacggcg cttaaaccctc 120
541 cgctgctcct gtaacccttg gaaacaacga cgtcgtattg tctgaagtta agcttttacgg 180
542 cgatgctcgt ttccggtaca taagttacaa aaatccgaac tatacatctt cctttttgcc 240
543 cgggttcgag cccgttgaaa agacgtcgtc gttttatgac cttgactacg gtatccgccg 300
544 tttggaccac gccgtaggaa cgtccctgag cttgcttcgg cagtggacta cgtgaaatca 360
545 ttcaccgat tccatgagtt cgccgaattc accgcggagg acgtcgggac gagcgagagg 420
546 gaactgaatt cggctgtttt agcttgcaac agtgagatgg tcttgattcc gatgaacgag 480
E--> 547 ccggtgtacg gaanaaaagg aagagccaga t 511 item 9
549 <210> SEQ ID NO: 18
550 <211> LENGTH: 170
551 <212> TYPE: PRT
552 <213> ORGANISM: Vernonia mesipifolia P.7
554 <400> SEQUENCE: 18
555 His Thr Asp Cys Arg Asn Phe Thr Ala Ser His Gly Leu Ala Val Arg
556 1 5 10 15
558 Ala Ile Ala Ile Glu Val Asp Asp Ala Glu Leu Ala Phe Ser Val Ser

```


RAW SEQUENCE LISTING

DATE: 02/13/2002

PATENT APPLICATION: US/09/857,613

TIME: 10:08:24

Input Set : A:\BB1289 PCT seq lst.txt

Output Set: N:\CRF3\02132002\I857613.raw

```

559          20          25          30
561 Val Ser His Gly Ala Lys Pro Ser Ala Ala Pro Val Thr Leu Gly Asn
562          35          40          45
564 Asn Asp Val Val Leu Ser Glu Val Lys Leu Tyr Gly Asp Val Ala Phe
565          50          55          60
567 Arg Tyr Ile Ser Tyr Lys Asn Pro Asn Tyr Thr Ser Ser Phe Leu Pro
568 65          70          75          80
570 Gly Phe Glu Pro Val Glu Lys Thr Ser Ser Phe Tyr Asp Leu Asp Tyr
571          85          90          95
573 Gly Ile Arg Arg Leu Asp His Ala Val Gly Asn Val Pro Glu Leu Ala
574          100          105          110
576 Ser Ala Val Asp Tyr Val Lys Ser Phe Thr Gly Phe His Glu Phe Ala
577          115          120          125
579 Glu Phe Thr Ala Glu Asp Val Gly Thr Ser Glu Arg Glu Leu Asn Ser
580          130          135          140
582 Val Val Leu Ala Cys Asn Ser Glu Met Val Leu Ile Pro Met Asn Glu
583 145          150          155          160
E--> 585 Pro Val Tyr Gly Xaa Lys Gly Arg Ala Arg
586          165          170
588 <210> SEQ ID NO: 19
589 <211> LENGTH: 1165
590 <212> TYPE: DNA
591 <213> ORGANISM: Triticum aestivum
593 <400> SEQUENCE: 19
594 caagaagcga acacacacca tgccgcccac cccaccacc cccgcagcca ccggcgccgc 60
595 cgcggtgacg cgggagcacg cgcgcccgcg ccgaatggtc cgcttcaacc cgcgagcga 120
596 cgcttccac acgctcgct tccaccacgt cgagttctgg tgcgcggacg ccgcctccgc 180
597 cgccggccgc ttgccttcg cgctcggcgc gccctcgcc gccaggtccg acctctccac 240
598 ggggaactcc gtgcacgcct cccagctgct ccgctcgggc aacctcgct tctcttcac 300
599 cgcgccctac gccaacggct ggcagccgc caccgcctcc ctgcccctcc tctccgcga 360
600 cgccgcgcgc cggttctccg cggaccacgg gctcgcggtg cgctccatag cgctgcgcgt 420
601 cgcgagcgc gccgagcct tccgcgccag cgtcgacggg ggcgcgcgc ccgccttcag 480
602 ccccgctggc ctcggccgcg gcttcggctt tgcggaggtc gacgtctac gcgacgtcgt 540
E--> 603 gctccgcttc gtcagcatcc ggacggnacg gacgtgcctt cttgccgggg ttccgaggcg 600
E--> 604 ttgagcaacc gggtgccgtg gactaanggc tgacacggnt tgacacgttg tccgnaagtc 660
E--> 605 cggagcttgc ttccggcccg cctaacgtag ccggctnaac gggttcaana attcgccagt 720
606 taacacggag gacgtgggca cggccgagag cgggctcaac tccatgggtg tccccaacaa 780
607 ctggaggggc gtgctgctgc cgtcaacga gccggtgcac ggcaccaagc gccggagcca 840
608 gatacagacg ttcttgaac accacggcgg ctcgggctg cagcacatcg cggtgccag 900
609 cagcgacgtg ctcaggacgc tcaggagat gcgtgcgcgc tccgccatgg gcggcttcga 960
610 cttcttgcga ccccgctgc cgaagtacta cgaaggcgtg cggcgcatcg ccggggatgt 1020
E--> 611 gctctcgag ggcgaatna agaatgcaa gaactggggg tgctcntcca caaggaagaa 1080
E--> 612 caaagggtgt tgctacaaat cctcaacaag ccaatntggg acaagccgac ttgttctggt 1140
E--> 613 agatattcac angatctggt gcatg 1165
1926 <210> SEQ ID NO: 43
1927 <211> LENGTH: 445
1928 <212> TYPE: PRT
1929 <213> ORGANISM: Arabidopsis thaliana
1931 <400> SEQUENCE: 43

```

item 9

item 9

item 9

P. 9

RAW SEQUENCE LISTING

DATE: 02/13/2002

PATENT APPLICATION: US/09/857,613

TIME: 10:08:25

Input Set : A:\BB1289 PCT seq 1st.txt

Output Set: N:\CRF3\02132002\I857613.raw

```

1932 Met Gly His Gln Asn Ala Ala Val Ser Glu Asn Gln Asn His Asp Asp
1933 1 5 10 15
1935 Gly Ala Ala Ser Ser Pro Gly Phe Lys Leu Val Gly Phe Ser Lys Phe
1936 20 25 30
1938 Val Arg Lys Asn Pro Lys Ser Asp Lys Phe Lys Val Lys Arg Phe His
1939 35 40 45
1941 His Ile Glu Phe Trp Cys Gly Asp Ala Thr Asn Val Ala Arg Arg Phe
1942 50 55 60
1944 Ser Trp Gly Leu Gly Met Arg Phe Ser Ala Lys Ser Asp Leu Ser Thr
1945 65 70 75 80
1947 Gly Asn Met Val His Ala Ser Tyr Leu Leu Thr Ser Gly Asp Leu Arg
1948 85 90 95
1950 Phe Leu Phe Thr Ala Pro Tyr Ser Pro Ser Leu Ser Ala Gly Glu Ile
1951 100 105 110
1953 Lys Pro Thr Thr Thr Ala Ser Ile Pro Ser Phe Asp His Gly Ser Cys
1954 115 120 125
1956 Arg Ser Phe Phe Ser Ser His Gly Leu Gly Val Arg Ala Val Ala Ile
1957 130 135 140
1959 Glu Val Glu Asp Ala Glu Ser Ala Phe Ser Ile Ser Val Ala Asn Gly
1960 145 150 155 160
1962 Ala Ile Pro Ser Ser Pro Pro Ile Val Leu Asn Glu Ala Val Thr Ile
1963 165 170 175
1965 Ala Glu Val Lys Leu Tyr Gly Asp Val Val Leu Arg Tyr Val Ser Tyr
1966 180 185 190
1968 Lys Ala Glu Asp Thr Glu Lys Ser Glu Phe Leu Pro Gly Phe Glu Arg
1969 195 200 205
1971 Val Glu Asp Ala Ser Ser Phe Pro Leu Asp Tyr Gly Ile Arg Arg Leu
1972 210 215 220
1974 Asp His Ala Val Gly Asn Val Pro Glu Leu Gly Pro Ala Leu Thr Tyr
1975 225 230 235 240
1977 Val Ala Gly Phe Thr Gly Phe His Gln Phe Ala Glu Phe Thr Ala Asp
1978 245 250 255
1980 Asp Val Gly Thr Ala Glu Ser Gly Leu Asn Ser Ala Val Leu Ala Ser
1981 260 265 270
1983 Asn Asp Glu Met Val Leu Leu Pro Ile Asn Glu Pro Val His Gly Thr
1984 275 280 285
1986 Lys Arg Lys Ser Gln Ile Gln Thr Tyr Leu Glu His Asn Glu Gly Ala
1987 290 295 300
1989 Gly Leu Gln His Leu Ala Leu Met Ser Glu Asp Ile Phe Arg Thr Leu
1990 305 310 315 320
1992 Arg Glu Met Arg Lys Arg Ser Ser Ile Gly Gly Phe Asp Phe Met Pro
1993 325 330 335
1995 Ser Pro Pro Pro Thr Tyr Tyr Gln Asn Leu Lys Lys Arg Val Gly Asp
1996 340 345 350
1998 Val Leu Ser Asp Asp Gln Ile Lys Glu Cys Glu Glu Leu Gly Ile Leu
1999 355 360 365
2001 Val Asp Arg Asp Asp Gln Gly Thr Leu Leu Gln Ile Phe Thr Lys Pro
2002 370 375 380
2004 Leu Gly Asp Arg Pro Thr Ile Phe Ile Glu Ile Ile Gln Arg Val Gly

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,613

DATE: 02/13/2002

TIME: 10:08:25

Input Set : A:\BB1289 PCT seq 1st.txt

Output Set: N:\CRF3\02132002\I857613.raw

[illegible]

FYE

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 02/13/2002

PATENT APPLICATION: US/09/857,613

TIME: 10:08:26

Input Set : A:\BB1289 PCT seq 1st.txt

Output Set: N:\CRF3\02132002\I857613.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:37 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:95 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
M:340 Repeated in SeqNo=3
L:135 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:166 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:289 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
M:340 Repeated in SeqNo=9
L:328 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
M:340 Repeated in SeqNo=10
L:376 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
M:340 Repeated in SeqNo=11
L:411 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
M:340 Repeated in SeqNo=13
L:442 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
L:464 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
M:340 Repeated in SeqNo=15
L:515 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
L:547 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
L:585 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:603 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19
M:340 Repeated in SeqNo=19
L:690 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:700 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:701 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:740 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
L:740 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:849 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:850 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:850 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:851 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:851 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:852 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:852 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:853 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:853 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1052 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29
L:1052 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1054 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29
L:1054 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1088 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:30

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/857,613

DATE: 02/13/2002

TIME: 10:08:26

Input Set : A:\BB1289 PCT seq lst.txt

Output Set : N:\CRF3\02132002\I857613.raw

L:1088 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:1094 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:30
L:1094 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:2016 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43